

SEQUENCE LISTING
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The Regents of the University of California

<120> Assays for Sensory Modulators Using a Sensory Cell
Specific G-Protein Alpha Subunit

<130> 02307E-092610US

<140> US 09/492,028

<141> 2000-01-26

<150> US 60/117,367

<151> 1999-01-27

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> Mus sp.

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<221> CDS

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<223> mouse taste cell specific G-protein alpha 14
subunit (TC-Galpha14)

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ctccaggtcc ctgtcgctcc gtcgagggtgg caagcc atg gcc ggc tgc tgc tgt 174
Met Ala Gly Cys Cys Cys
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Leu Ser Ala Glu Glu Lys Glu Ser Gln Arg Ile Ser Ala Glu Ile Glu
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Arg His Val Arg Arg Asp Lys Lys Asp Ala Arg Arg Glu Leu Lys Leu
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Leu Leu Leu Gly Thr Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln
40 45 50atg agg ata atc cat ggg tct ggc tac agt gat gaa gat aga aag ggc 366
Met Arg Ile Ile His Gly Ser Gly Tyr Ser Asp Glu Asp Arg Lys Gly
55 60 65 70ttc acg aag ctg gtt tac caa aac ata ttc acg gcc atg caa gcc atg 414
Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe Thr Ala Met Gln Ala Met
75 80 85

atc	aga	gca	atg	gat	acc	ctg	agg	ata	caa	taa	atg	tgt	gag	cag	aat	462
Ile	Arg	Ala	Met	Asp	Thr	Leu	Arg	Ile	Gln	Tyr	Met	Cys	Glu	Gln	Asn	
90								95					100			
aag	gaa	aat	gcc	cag	atc	atc	agg	gaa	gtg	gaa	gta	gac	aag	gtc	act	510
Lys	Glu	Asn	Ala	Gln	Ile	Ile	Arg	Glu	Val	Glu	Val	Asp	Lys	Val	Thr	
105							110					115				
gca	ctc	tct	aga	gac	cag	gtg	gca	gcc	atc	aag	cag	ctg	tgg	ctg	gat	558
Ala	Leu	Ser	Arg	Asp	Gln	Val	Ala	Ala	Ile	Lys	Gln	Leu	Trp	Leu	Asp	
120							125					130				
ccc	gga	atc	cag	gag	tgt	tac	gac	agg	agg	agg	gag	tac	cag	ctg	tca	606
Pro	Gly	Ile	Gln	Glu	Cys	Tyr	Asp	Arg	Arg	Arg	Glu	Tyr	Gln	Leu	Ser	
135							140				145		150			
gac	tct	gcc	aaa	tat	tac	ctg	acg	gac	att	gag	cgt	atc	gcc	atg	ccc	654
Asp	Ser	Ala	Lys	Tyr	Tyr	Leu	Thr	Asp	Ile	Glu	Arg	Ile	Ala	Met	Pro	
155							160					165				
tct	ttc	gtg	cca	aca	caa	cag	gat	gtg	ctt	cgt	gtt	aga	gtg	ccc	acc	702
Ser	Phe	Val	Pro	Thr	Gln	Gln	Asp	Val	Leu	Arg	Val	Arg	Val	Pro	Thr	
170							175					180				
act	ggc	atc	ata	gaa	tat	cca	ttc	gac	ctg	gaa	aac	atc	atc	ttc	cga	750
Thr	Gly	Ile	Ile	Glu	Tyr	Pro	Phe	Asp	Leu	Glu	Asn	Ile	Ile	Phe	Arg	
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Met	Val	Asp	Val	Gly	Gly	Gln	Arg	Ser	Glu	Arg	Arg	Lys	Trp	Ile	His	
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tgc	ttt	gag	agt	gtc	acc	tcc	atc	att	ttc	ttg	gtt	gct	ctg	agt	gaa	846
Cys	Phe	Glu	Ser	Val	Thr	Ser	Ile	Ile	Phe	Leu	Val	Ala	Leu	Ser	Glu	
215							220			225			230			
tat	gac	cag	gtt	ctg	gct	gag	tgt	gac	aat	gag	aac	cgc	atg	gag	gag	894
Tyr	Asp	Gln	Val	Leu	Ala	Glu	Cys	Asp	Asn	Glu	Asn	Arg	Met	Glu	Glu	
235							240					245				
agc	aaa	gcc	ctg	ttt	aga	acc	atc	atc	acc	taa	ccc	tgg	ttt	ctg	aac	942
Ser	Lys	Ala	Leu	Phe	Arg	Thr	Ile	Ile	Thr	Tyr	Pro	Trp	Phe	Leu	Asn	
250							255					260				
tcc	tcc	gtg	att	ctg	ttc	tta	aac	aag	aag	gat	ctt	cta	gag	gag	aaa	990
Ser	Ser	Val	Ile	Leu	Phe	Leu	Asn	Lys	Lys	Asp	Leu	Leu	Glu	Glu	Lys	
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atc	atg	taa	tct	cat	cta	att	agc	taa	ttc	cca	gag	taa	aca	gga	cca	1038
Ile	Met	Tyr	Ser	His	Leu	Ile	Ser	Tyr	Phe	Pro	Glu	Tyr	Thr	Gly	Pro	
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aag	caa	gat	gtc	aaa	gca	gcc	agg	gac	ttt	atc	ctg	aag	ctg	tat	caa	1086
Lys	Gln	Asp	Val	Lys	Ala	Ala	Arg	Asp	Phe	Ile	Leu	Lys	Leu	Tyr	Gln	
295							300				305		310			
gac	cag	aat	cct	gac	aaa	gag	aag	gtt	atc	taa	tct	cac	ttc	act	tgt	1134
Asp	Gln	Asn	Pro	Asp	Lys	Glu	Lys	Val	Ile	Tyr	Ser	His	Phe	Thr	Cys	
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gct aca gac acc gag aat atc cgc ttt gtg ttt gct gct gtc aaa gac	1182
Ala Thr Asp Thr Glu Asn Ile Arg Phe Val Phe Ala Ala Val Lys Asp	
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340	
aca atc cta cag cta aac cta cg ^g gag ttc aac ttg gtg taa	1224
Thr Ile Leu Gln Leu Asn Leu Arg Glu Phe Asn Leu Val	
345	350
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gtgcttctgg accaggacct aaggacatta tgtagccac aggacagaga tggtagtgc	1344
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Asp Glu Asp Arg Lys Gly Phe Thr Lys Leu Val Tyr Gln Asn Ile Phe	
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Thr Ala Met Gln Ala Met Ile Arg Ala Met Asp Thr Leu Arg Ile Gln	
85 90 95	
Tyr Met Cys Glu Gln Asn Lys Glu Asn Ala Gln Ile Ile Arg Glu Val	
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Glu Val Asp Lys Val Thr Ala Leu Ser Arg Asp Gln Val Ala Ala Ile	
115 120 125	
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Arg Glu Tyr Gln Leu Ser Asp Ser Ala Lys Tyr Tyr Leu Thr Asp Ile	
145 150 155 160	
Glu Arg Ile Ala Met Pro Ser Phe Val Pro Thr Gln Gln Asp Val Leu	
165 170 175	
Arg Val Arg Val Pro Thr Thr Gly Ile Ile Glu Tyr Pro Phe Asp Leu	
180 185 190	
Glu Asn Ile Ile Phe Arg Met Val Asp Val Gly Gly Gln Arg Ser Glu	
195 200 205	
Arg Arg Lys Trp Ile His Cys Phe Glu Ser Val Thr Ser Ile Ile Phe	
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Leu Val Ala Leu Ser Glu Tyr Asp Gln Val Leu Ala Glu Cys Asp Asn	
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Glu Asn Arg Met Glu Glu Ser Lys Ala Leu Phe Arg Thr Ile Ile Thr	
245 250 255	
Tyr Pro Trp Phe Leu Asn Ser Ser Val Ile Leu Phe Leu Asn Lys Lys	
260 265 270	
Asp Leu Leu Glu Glu Lys Ile Met Tyr Ser His Leu Ile Ser Tyr Phe	
275 280 285	

Pro Glu Tyr Thr Gly Pro Lys Gln Asp Val Lys Ala Ala Arg Asp Phe
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Ile Leu Lys Leu Tyr Gln Asp Gln Asn Pro Asp Lys Glu Lys Val Ile
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Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Glu Asn Ile Arg Phe Val
325 330 335
Phe Ala Ala Val Lys Asp Thr Ile Leu Gln Leu Asn Leu Arg Glu Phe
340 345 350
Asn Leu Val
355